AMENDMENTS

In the specification:

On page 8, please amend the paragraph on lines 18-28 as follows:

[Figure 11 shows] Figures 11A to 11E show a sequence alignment [(SEQ ID NOS:1-17, respectively)] made from a structural overlay of pharmacofamily 1. The corresponding SEQ ID NOS are: 1AGN (SEQ ID NO:1); 1AXE (SEQ ID NO:2); 1YKF (SEQ ID NO:3); 1HYH (SEQ ID NO:4); 1LDN (SEQ ID NO:5); 1EMD (SEQ ID NO:6); 9LDB (SEQ ID NO:7); 4MDH (SEQ ID NO:8); 1BMD (SEQ ID NO:9); 1PSD (SEQ ID NO:10); 1DXY (SEQ ID NO:11); 2NAD (SEQ ID NO:12); 1A4I (SEQ ID NO:13); 1B3R (SEQ ID NO:14); 1PJC (SEQ ID NO:15); 1ARZ (SEQ ID NO:16); 1QR6 (SEQ ID NO:17). Amino acids shown correspond to those which are within regions that overlap in the structural overlay. All bolded letters are within 4.5 Angstroms from a ligand binding site. Underlining indicates proximity to a cofactor ligand and/or substrate ligand as follows: bold underling indicates proximity to a bound cofactor, double underling indicates proximity to a bound substrate, and dotted underling indicates proximity to both bound cofactor and bound substrate.